
Gene expression commons: an open platform for absolute gene expression profiling.

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Public Summary:

A new software program enables researchers to see the whole picture of gene expression in a sample. The program, called Gene Expression Commons, is publicly available at <https://gexc.stanford.edu/>. Its developers expect it to transform studies of gene expression. Gene Expression Commons overcomes an inherent shortcoming of microarray technology: the fact that experimental results are delivered as relative differences in gene expression within individual experiments, rather than absolute values that can be compared in concert among many samples. We analyzed collections of thousands of publicly available DNA microarray experiments. About 25,000 of the experiments had been performed with human data; 10,000 with data from mice. Individually, each dataset suffered from the same drawbacks described above. But together they can be viewed as a continuum, or a stable common reference. The resulting Gene Expression Commons maps data submitted by the user onto this common reference, and returns absolute expression levels that can then be compared among many combinations of samples. To demonstrate an application of Gene Expression Commons, the Weissman group generated microarray data on 39 highly purified distinct cell types in the blood and immune system and then submitted these data to the program. Now any researcher can explore the expression pattern of any gene in the blood and immune system with just a few clicks of a computer mouse. The Gene Expression Commons is designed as an open-platform, so new users can input data themselves. A neurologist, for example, may want to analyze data from microarrays conducted on cells of the nervous system. And the Gene Expression Commons is open not only for DNA microarray technology. This "common reference" strategy should work well for any type of high-throughput data.

Scientific Abstract:

Gene expression profiling using microarrays has been limited to comparisons of gene expression between small numbers of samples within individual experiments. However, the unknown and variable sensitivities of each probeset have rendered the absolute expression of any given gene nearly impossible to estimate. We have overcome this limitation by using a very large number (>10,000) of varied microarray data as a common reference, so that statistical attributes of each probeset, such as the dynamic range and threshold between low and high expression, can be reliably discovered through meta-analysis. This strategy is implemented in a web-based platform named "Gene Expression Commons" (<https://gexc.stanford.edu/>) which contains data of 39 distinct highly purified mouse hematopoietic stem/progenitor/differentiated cell populations covering almost the entire hematopoietic system. Since the Gene Expression Commons is designed as an open platform, investigators can explore the expression level of any gene, search by expression patterns of interest, submit their own microarray data, and design their own working models representing biological relationship among samples.

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